



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/082,018A

DATE: 09/16/2004

TIME: 15:58:28

Input Set : A:\10275-133001.TXT

Output Set: N:\CRF4\09162004\J082018A.raw

4 <110> APPLICANT: Chen, Li How
 5 Meade, Harry M.
 8 <120> TITLE OF INVENTION: NOVEL MODIFIED MSP-1 NUCLEIC ACID
 9 SEQUENCES AND METHODS FOR INCREASING MRNA LEVELS AND PROTEIN
 10 EXPRESSION IN CELL SYSTEMS
 13 <130> FILE REFERENCE: 10275-133001
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/082,018A
 C--> 16 <141> CURRENT FILING DATE: 2002-02-20
 18 <150> PRIOR APPLICATION NUMBER: US 60/085,649
 19 <151> PRIOR FILING DATE: 1998-05-15
 21 <150> PRIOR APPLICATION NUMBER: US 60/062,592
 22 <151> PRIOR FILING DATE: 1997-10-20
 24 <160> NUMBER OF SEQ ID NOS: 19
 26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 1065
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Plasmodium falciparum
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (1)...(1065)
 37 <400> SEQUENCE: 1

38 gcc gtc act ccc tcc gtc atc gat aac atc ctg tcc aag atc gag aac	48
39 Ala Val Thr Pro Ser Val Ile Asp Asn Ile Leu Ser Lys Ile Glu Asn	
40 1 5 10 15	
42 gag tac gag gtg ctg tac ctg aag ccg ctg gca ggg gtc tac cgg agc	96
43 Glu Tyr Glu Val Leu Tyr Leu Lys Pro Leu Ala Gly Val Tyr Arg Ser	
44 20 25 30	
46 ctg aag aag cag ctg gag aac aac gtg atg acc ttc aac gtg aac gtg	144
47 Leu Lys Lys Gln Leu Glu Asn Asn Val Met Thr Phe Asn Val Asn Val	
48 35 40 45	
50 aag gat atc ctg aac agc cgg ttc aac aag cgg gag aac ttc aag aac	192
51 Lys Asp Ile Leu Asn Ser Arg Phe Asn Lys Arg Glu Asn Phe Lys Asn	
52 50 55 60	
54 gtg ctg gag agc gat ctg atc ccc tac aag gat ctg acc agc agc aac	240
55 Val Leu Glu Ser Asp Leu Ile Pro Tyr Lys Asp Leu Thr Ser Ser Asn	
56 65 70 75 80	
58 tac gtg gtc aag gat ccc tac aag ttc ctg aac aag gag aag aga gat	288
59 Tyr Val Val Lys Asp Pro Tyr Lys Phe Leu Asn Lys Glu Lys Arg Asp	
60 85 90 95	
62 aag ttc ctg agc agt tac aac tac atc aag gat agc att gat acc gat	336
63 Lys Phe Leu Ser Ser Tyr Asn Tyr Ile Lys Asp Ser Ile Asp Thr Asp	
64 100 105 110	



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66 atc aac ttc gcc aac gat gtc ctg gga tac tac aag atc ctg tcc gag      384
67 Ile Asn Phe Ala Asn Asp Val Leu Gly Tyr Tyr Lys Ile Leu Ser Glu
68      115      120      125
70 aag tac aag agc gat ctg gat tca atc aag aag tac atc aac gat aag      432
71 Lys Tyr Lys Ser Asp Leu Asp Ser Ile Lys Lys Tyr Ile Asn Asp Lys
72      130      135      140
74 cag gga gag aac gag aag tac ctg ccc ttc ctg aac aac atc gag acc      480
75 Gln Gly Glu Asn Glu Lys Tyr Leu Pro Phe Leu Asn Asn Ile Glu Thr
76 145      150      155      160
78 ctg tac aag acc gtc aac gat aag att gat ctg ttc gtg atc cac ctg      528
79 Leu Tyr Lys Thr Val Asn Asp Lys Ile Asp Leu Phe Val Ile His Leu
80      165      170      175
82 gag gcc aag gtc ctg aac tac aca tat gag aag agc aac gtg gag gtc      576
83 Glu Ala Lys Val Leu Asn Tyr Thr Tyr Glu Lys Ser Asn Val Glu Val
84      180      185      190
86 aag atc aag gag ctg aat tac ctg aag acc atc cag gat aag ctg gcc      624
87 Lys Ile Lys Glu Leu Asn Tyr Leu Lys Thr Ile Gln Asp Lys Leu Ala
88      195      200      205
90 gat ttc aag aag aac aac aac ttc gtc ggg atc gcc gat ctg agc acc      672
91 Asp Phe Lys Lys Asn Asn Asn Phe Val Gly Ile Ala Asp Leu Ser Thr
92      210      215      220
94 gat tac aac cac aac aac ctg ctg acc aag ttc ctg agc acc ggt atg      720
95 Asp Tyr Asn His Asn Asn Leu Leu Thr Lys Phe Leu Ser Thr Gly Met
96 225      230      235      240
98 gtc ttc gaa aac ctg gcc aag acc gtc ctg agc aac ctg ctg gat ggg      768
99 Val Phe Glu Asn Leu Ala Lys Thr Val Leu Ser Asn Leu Leu Asp Gly
100      245      250      255
102 aac ctg cag ggg atg ctg aac atc agc cag cac cag tgt gtg aag aag      816
103 Asn Leu Gln Gly Met Leu Asn Ile Ser Gln His Gln Cys Val Lys Lys
104      260      265      270
106 cag tgt ccc cag aac agc ggg tgt ttc aga cac ctg gat gag aga gag      864
107 Gln Cys Pro Gln Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu
108      275      280      285
110 gag tgt aag tgt ctg ctg aac tac aag cag gaa ggt gat aag tgt gtg      912
111 Glu Cys Lys Cys Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val
112      290      295      300
114 gaa aac ccc aat cct act tgt aac gag aac aat ggt gga tgt gat gcc      960
115 Glu Asn Pro Asn Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala
116 305      310      315      320
118 gat gcc aag tgt acc gag gag gat tca ggg agc aac ggg aag aag atc      1008
119 Asp Ala Lys Cys Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile
120      325      330      335
122 acc tgt gag tgt acc aag cct gat tct tat cca ctg ttc gat ggt atc      1056
123 Thr Cys Glu Cys Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile
124      340      345      350
126 ttc tgt agt      1065
127 Phe Cys Ser
128      355
131 <210> SEQ ID NO: 2

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132 <211> LENGTH: 1088
133 <212> TYPE: DNA
134 <213> ORGANISM: Plasmodium falciparum
136 <220> FEATURE:
137 <221> NAME/KEY: CDS
138 <222> LOCATION: (1)...(1083)
140 <400> SEQUENCE: 2
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142 Ala Val Thr Pro Ser Val Ile Asp Asn Ile Leu Ser Lys Ile Glu Asn
143 1 5 10 15
145 gaa tat gag gtt tta tat tta aaa cct tta gca ggt gtt tat aga agt      96
146 Glu Tyr Glu Val Leu Tyr Leu Lys Pro Leu Ala Gly Val Tyr Arg Ser
147 20 25 30
149 tta aaa aaa caa tta gaa aat aac gtt atg aca ttt aat gtt aat gtt      144
150 Leu Lys Lys Gln Leu Glu Asn Asn Val Met Thr Phe Asn Val Asn Val
151 35 40 45
153 aag gat att tta aat tca cga ttt aat aaa cgt gaa aat ttc aaa aat      192
154 Lys Asp Ile Leu Asn Ser Arg Phe Asn Lys Arg Glu Asn Phe Lys Asn
155 50 55 60
157 gtt tta gaa tca gat tta att cca tat aaa gat tta aca tca agt aat      240
158 Val Leu Glu Ser Asp Leu Ile Pro Tyr Lys Asp Leu Thr Ser Ser Asn
159 65 70 75 80
161 tat gtt gtc aaa gat cca tat aaa ttt ctt aat aaa gaa aaa aga gat      288
162 Tyr Val Val Lys Asp Pro Tyr Lys Phe Leu Asn Lys Glu Lys Arg Asp
163 85 90 95
165 aaa ttc tta agc agt tat aat tat att aag gat tca ata gat acg gat      336
166 Lys Phe Leu Ser Ser Tyr Asn Tyr Ile Lys Asp Ser Ile Asp Thr Asp
167 100 105 110
169 ata aat ttt gca aat gat gtt ctt gga tat tat aaa ata tta tcc gaa      384
170 Ile Asn Phe Ala Asn Asp Val Leu Gly Tyr Tyr Lys Ile Leu Ser Glu
171 115 120 125
173 aaa tat aaa tca gat tta gat tca att aaa aaa tat atc aac gac aaa      432
174 Lys Tyr Lys Ser Asp Leu Asp Ser Ile Lys Lys Tyr Ile Asn Asp Lys
175 130 135 140
177 caa ggt gaa aat gag aaa tac ctt ccc ttt tta aac aat att gag acc      480
178 Gln Gly Glu Asn Glu Lys Tyr Leu Pro Phe Leu Asn Asn Ile Glu Thr
179 145 150 155 160
181 tta tat aaa aca gtt aat gat aaa att gat tta ttt gta att cat tta      528
182 Leu Tyr Lys Thr Val Asn Asp Lys Ile Asp Leu Phe Val Ile His Leu
183 165 170 175
185 gaa gca aaa gtt cta aat tat aca tat gag aaa tca aac gta gaa gtt      576
186 Glu Ala Lys Val Leu Asn Tyr Thr Tyr Glu Lys Ser Asn Val Glu Val
187 180 185 190
189 aaa ata aaa gaa ctt aat tac tta aaa aca att caa gac aaa ttg gca      624
190 Lys Ile Lys Glu Leu Asn Tyr Leu Lys Thr Ile Gln Asp Lys Leu Ala
191 195 200 205
193 gat ttt aaa aaa aat aac aat ttc gtt gga att gct gat tta tca aca      672
194 Asp Phe Lys Lys Asn Asn Asn Phe Val Gly Ile Ala Asp Leu Ser Thr
195 210 215 220

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197 gat tat aac cat aat aac tta ttg aca aag ttc ctt agt aca ggt atg      720
198 Asp Tyr Asn His Asn Asn Leu Leu Thr Lys Phe Leu Ser Thr Gly Met
199 225                      230                      235                      240
201 gtt ttt gaa aat ctt gct aaa acc gtt tta tct aat tta ctt gat gga      768
202 Val Phe Glu Asn Leu Ala Lys Thr Val Leu Ser Asn Leu Leu Asp Gly
203                      245                      250                      255
205 aac ttg caa ggt atg tta aac att tca caa cac caa tgc gta aaa aaa      816
206 Asn Leu Gln Gly Met Leu Asn Ile Ser Gln His Gln Cys Val Lys Lys
207                      260                      265                      270
209 caa tgt cca caa aat tct gga tgt ttc aga cat tta gat gaa aga gaa      864
210 Gln Cys Pro Gln Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu
211                      275                      280                      285
213 gaa tgt aaa tgt tta tta aat tac aaa caa gaa ggt gat aaa tgt gtt      912
214 Glu Cys Lys Cys Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val
215                      290                      295                      300
217 gaa aat cca aat cct act tgt aac gaa aat aat ggt gga tgt gat gca      960
218 Glu Asn Pro Asn Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala
219 305                      310                      315                      320
221 gat gcc aaa tgt acc gaa gaa gat tca ggt agc aac gga aag aaa atc      1008
222 Asp Ala Lys Cys Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile
223                      325                      330                      335
225 aca tgt gaa tgt act aaa cct gat tct tat cca ctt ttc gat ggt att      1056
226 Thr Cys Glu Cys Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile
227                      340                      345                      350
229 ttc tgc agt cac cac cac cac cac cac taact      1088
230 Phe Cys Ser His His His His His His
231                      355                      360
234 <210> SEQ ID NO: 3
235 <211> LENGTH: 88
236 <212> TYPE: DNA
237 <213> ORGANISM: Plasmodium falciparum
239 <400> SEQUENCE: 3
240 tcgacgagag ccatgaaggt cctcatcctt gcctgtctgg tggctctggc cattgcaaga      60
241 gagcaggaag aactcaatgt agtcggta      88
243 <210> SEQ ID NO: 4
244 <211> LENGTH: 88
245 <212> TYPE: DNA
246 <213> ORGANISM: Plasmodium falciparum
248 <400> SEQUENCE: 4
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252 <210> SEQ ID NO: 5
253 <211> LENGTH: 60
254 <212> TYPE: DNA
255 <213> ORGANISM: Plasmodium falciparum
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260 <210> SEQ ID NO: 6
261 <211> LENGTH: 48

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262 <212> TYPE: DNA
263 <213> ORGANISM: Plasmodium falciparum
265 <400> SEQUENCE: 6
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268 <210> SEQ ID NO: 7
269 <211> LENGTH: 31
270 <212> TYPE: DNA
271 <213> ORGANISM: Plasmodium falciparum
273 <400> SEQUENCE: 7
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276 <210> SEQ ID NO: 8
277 <211> LENGTH: 1142
278 <212> TYPE: DNA
279 <213> ORGANISM: Plasmodium falciparum
281 <220> FEATURE:
282 <221> NAME/KEY: CDS
283 <222> LOCATION: (1)...(1142)
285 <400> SEQUENCE: 8
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287 Met Lys Val Leu Ile Ile Ala Cys Leu Val Ala Leu Ala Ile Ala Ala
288 1 5 10 15
290 gtc act ccc tcc gtc atc gat aac atc ctg tcc aag atc gag aac gag 96
291 Val Thr Pro Ser Val Ile Asp Asn Ile Leu Ser Lys Ile Glu Asn Glu
292 20 25 30
294 tac gag gtg ctg tac ctg aag ccc ctg gca gga gtc tac agg agc ctg 144
295 Tyr Glu Val Leu Tyr Leu Lys Pro Leu Ala Gly Val Tyr Arg Ser Leu
296 35 40 45
298 aag aag cag ctg gag aac aac gtg atg acc ttc aac gtg aac gtg aag 192
299 Lys Lys Gln Leu Glu Asn Asn Val Met Thr Phe Asn Val Asn Val Lys
300 50 55 60
302 gat atc ctg aac agc agg ttc aac aag agg gag aac ttc aag aac gtg 240
303 Asp Ile Leu Asn Ser Arg Phe Asn Lys Arg Glu Asn Phe Lys Asn Val
304 65 70 75 80
306 ctg gag agc gat ctg atc ccc tac aag gat ctg acc agc agc aac tac 288
307 Leu Glu Ser Asp Leu Ile Pro Tyr Lys Asp Leu Thr Ser Ser Asn Tyr
308 85 90 95
310 gtg gtc aaa gat ccc tac aag ttc ctg aac aag gag aag aga gat aag 336
311 Val Val Lys Asp Pro Tyr Lys Phe Leu Asn Lys Glu Lys Arg Asp Lys
312 100 105 110
314 ttc ctg agc agt tac aat tac atc aag gat agc att gac acc gat atc 384
315 Phe Leu Ser Ser Tyr Asn Tyr Ile Lys Asp Ser Ile Asp Thr Asp Ile
316 115 120 125
318 aac ttc gcc aac gat gtc ctg gga tac tac aag atc ctg tcc gag aag 432
319 Asn Phe Ala Asn Asp Val Leu Gly Tyr Tyr Lys Ile Leu Ser Glu Lys
320 130 135 140
322 tac aag agc gat ctg gat agc atc aag aag tac atc aac gat aag cag 480
323 Tyr Lys Ser Asp Leu Asp Ser Ile Lys Lys Tyr Ile Asn Asp Lys Gln
324 145 150 155 160
326 gga gag aac gag aag tac ctg ccc ttc ctg aac aac atc gag acc ctg 528

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VERIFICATION SUMMARY

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Input Set : A:\10275-133001.TXT

Output Set: N:\CRF4\09162004\J082018A.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application Number
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date